

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:27:49 ; Search time 2530.16 Seconds
(without alignments)
10849.659 Million cell updates/sec

Title: US-09-856-979-6

Perfect score: 1695

Sequence: 1 ccgcagatctctgtgtga.....tccatcaagcgcgcgatg 1695

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba.*
 - 2: em_esthma.*
 - 3: em_estin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pln.*
 - 21: em_gss_vrt.*
 - 22: em_gss_fun.*
 - 23: em_gss_mam.*
 - 24: em_gss_mus.*
 - 25: em_gss_other.*
 - 26: em_gss_pro.*
 - 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	187.4	11.1	948	17	AQ329933
c 2	178.8	10.5	668	17	BH878425
c 3	87	5.1	331	9	AL371988
c 4	85.8	5.1	415	17	BH885023
c 5	82.2	4.8	120	17	BH416345
c 6	78.6	4.6	654	14	B0014814

c 7	78.6	4.6	655	14	B0854032
c 8	78.6	4.6	670	14	B0010172
c 9	78.6	4.6	712	14	B0000882
c 10	78.6	4.6	732	14	B0012310
c 11	78.6	4.6	744	14	B0014761
c 12	78.6	4.6	745	14	B0850661
c 13	78.6	4.6	750	14	BQ933006
c 14	78.6	4.6	762	14	BQ853513
c 15	78	4.6	512	12	BG462180
c 16	78	4.6	607	14	BQ294181
c 17	78	4.6	642	14	B0037560
c 18	77	4.5	756	14	BQ839445
c 19	76.8	4.5	546	12	BF421436
c 20	76.6	4.5	167	17	AG024921
c 21	76.2	4.5	653	9	AI162258
c 22	76	4.5	523	10	AW011614
c 23	75.6	4.5	728	13	BM157838
c 24	75.4	4.4	497	13	BI644131
c 25	75.4	4.4	603	10	BE590288
c 26	75.4	4.4	625	12	BE942189
c 27	75.4	4.4	626	14	B0036825
c 28	75.4	4.4	629	12	BE942188
c 29	75.2	4.4	523	13	BI127466
c 30	75.2	4.4	555	10	BE499732
c 31	75.2	4.4	561	13	BM188325
c 32	75.2	4.4	642	10	BE229756
c 33	75.2	4.4	660	14	BQ294680
c 34	74.8	4.4	337	12	BF145411
c 35	74.8	4.4	344	9	AJ499862
c 36	74.8	4.4	869	12	BG345098
c 37	74.4	4.4	600	14	BQ149587
c 38	73.8	4.4	406	10	BE407080
c 39	73.8	4.4	512	10	AW282484
c 40	73.8	4.4	570	10	AV933056
c 41	73.8	4.4	582	10	AV932088
c 42	73.8	4.4	592	10	AV934263
c 43	73.8	4.4	666	13	BJ472315
c 44	73.8	4.4	941	14	BM817125
c 45	73.8	4.4	1116	11	AY103934

ALIGNMENTS

RESULT 1
AQ329933/c
LOCUS AQ329933 948 bp DNA linear GSS 08-JAN-1999
DEFINITION nbxb0046A15r CUGI Rice BAC Library Oryza sativa genomic clone
ACCESSION nbxb0046A15r, DNA sequence.
VERSION AQ329933
KEYWORDS AQ329933.1 GI:4121783
SOURCE GSS.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
Wing, R.A. and Dean, R.A.
1 (bases 1 to 948)
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 96.
Location/Qualifiers
1. .948

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nxb0046A15r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/notes="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
BASE COUNT 137 a 343 c 119 g 348 t 1 others
ORIGIN

Query Match 11.1%; Score 187.4; DB 17; Length 948;
Best Local Similarity 96.5%; Pred. No. 2.5e-43;
Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 727 ACATGCAGACAGACCATATCATGTTGCCCGCAGCAGACCCCGCAGATGAAGTTCCTG 786
DB 198 ACCTAGGACAGAGCCAGATCAATGATGATGATGATGATGATGATGATGATGATG 139
QY 787 TTCTCCACAGCAGATATCCGCACTGCGTCCCAACAAATGAAATCCAAAACCCACA 846
DB 138 TTCTCCACAGCAGATATCCGCACTGCGTCCCAACAAATGAAATCCAAAACCCACA 79
QY 847 TCGGCTCAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 906
DB 78 TCGGCTCAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 19
QY 907 ATAATAATAGCACACCTT 924
DB 18 ATAATAATAGCACACCTT 1

RESULT 2
BH878425 668 bp DNA linear GSS 05-AUG-2002
LOCUS hs82a08.b1 WGS-zmaysF (JM107 adapted methyl filtered) Zea mays
DEFINITION genomic clone hs82a08 5', DNA sequence.
ACCESSION BH878425
VERSION 1
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 668)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Katzenburger,F., King,L., Miller,B., Muller,S.,
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
```

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hs82 row: a Column: 08

Seq primer: -21M13UnivFwd

Class: shotgun

High quality sequence stop: 668.

Location/Qualifiers

FEATURES

source

1..668

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="hs82a08"

/clone_lib="WGS-zmaysF (JM107 adapted methyl filtered)"

/lab_host="JM107 or DH5a"

/notes="Organ: Immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

BASE COUNT 174 a 171 c 193 g 130 t

ORIGIN

Query Match 10.5%; Score 178.8; DB 17; Length 668;

Best Local Similarity 59.7%; Pred. No. 7.1e-41;

Matches 319; Conservative 0; Mismatches 212; Indels 3; Gaps 1;

QY 295 GACAATGTTGCACCTGGAACCTGTCATGTTTTTACATCTCTATTAAAGTAGCAAGGA 354

DB 128 GCGAGTATTTACTGTCGTAGGATCTGGCAATGGCACTCAAAACCAAGCAAA 187

QY 355 GTAGATTTATTTACAGAGAGAAATCTCTTCAGATCTTTCCACATGCAATGTCGTAA 414

DB 188 GCACAGAAATTTACCATGAGAACTCTTTGAGATCTTCCCGCAGCAGCGTGTAGA 247

QY 415 GAACAGATACATGTCAGCTTAGTTTGTATGACGGTCAATGCCATTTCTCTGAAGGCA 474

DB 248 GCAGGATACAAAGTGAAGCAGTCTGTATGTTGTCGCCGCGCAGCTTCTCTGAAGCG 307

QY 475 GTTCAGAGATCATGTTCTGGGATCTTGGAGGGCCCTGAAATTCGGAAACAGCTTAGT 534

DB 308 GTTCAGAAACCATCCCTCCGGGATCTGTGGAGCGCCCTGCAGCGGAAGACGAGAGGT 367

QY 535 TCAGTTTTAGTACCTAATGCTTTCGGTTTATCTACGTGAATGCCATTTCTGTAAAGCTGA 594

DB 368 TAAAGATGAGACTTCTCGACTCAACAGCTGTGTAGGTGCTAGCTGTAGCTGCAGA 427

QY 595 GTTTTCTACCATCTCCACAGCAATTAAGCTAATACCTGTCCAAAGAGTGGTGGCATTTT 654

DB 428 ACCTTCGACGCCATGGCGTGGCAGCAACGCA---ACCTGTCAAGGAGAGCGCGCGTTG 484

QY 655 GACCAATGAAGATCACAAGCATGGCAAGAAATGGCAATCTGGCAAGAGCGGAATATA 714

DB 485 GACCAGACGAAGACGAGCAGCATCCCGAGCAGCGCGTGGCAAAAGGAGCGTCAACACG 544

QY 715 TTGTATCTTACTACATCAACAGCAATATCAATGTTGGCCCGCAGCAAGGACCCCGCA 774

DB 545 TTGTACTCCGCGCATGTCACAGCAACGAGACGAGCGTCCCGCCCGGAGGATCCCGCT 604

QY 775 GATAAGTTCTCTGTTTCTCCACAGCAATATCCGCAACTGTCATAGTCCCAACA 828

DB 605 GACAGGTTCTCTGTTTCTCCATAGCAGGACGTCGAGACTGAAGAGAGACCCAAA 658

RESULT 3

AL371988/c

LOCUS

DEFINITION MCBAA47H04.F1 M8A Medicago truncatula cDNA clone MCBAA47H04 T3, mRNA

sequence.

331 bp

mRNA

linear

EST 03-AUG-2000

```

ACCESSION      AL371988
VERSION        AL371988.1  GI:9671741
KEYWORDS       EST.
SOURCE         barrel medic.
ORGANISM       Medicago truncatula
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots:
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
               Medicago.
REFERENCE      1 (bases 1 to 331)
AUTHORS       Journet,B.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
               Niebel,A., Carreau,V., Chacagnier,O., Kahn,D., Gianinazzi-Pearson
               V. and Gamas,P.
TITLE         Medicago truncatula ESTs from nitrogen-starved roots
JOURNAL       Unpublished (2000)
COMMENT       Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
               Biologie Moleculaire des Relations Plantes-Microorganismes,
               CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
               Mt-est@toulouse.inra.fr Website :
               http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES      Location/Qualifiers
               source
               1..331
               /organism="Medicago truncatula"
               /cultivar="Jemalong"
               /db_xref="taxon:3880"
               /clone_lib="MtBA47H04"
               /tissue_type="root tips"
               /dev_stage="harvested after 3 days of N-starvation"
               /note="Vector: pBluescript pSK; Site 1: EcoRI; Site 2:
               XhoI; Plants were grown in an aeroponic chamber for 14
               days on nitrogen-rich medium followed by 3 days on N-free
               medium. RNA was extracted from root tips (1-3 cm). cDNA
               was prepared from polyA+ enriched RNA. The cDNA was
               directionally ligated into Uni-zapXX vector from
               Stratagene and packaged using GigaPack Gold packaging
               extracts. Plasmids containing cDNA inserts were
               mass-excised from phage stocks using EXAssit helper phage
               and propagated in SOLR cells. Clone ordering and
               sequencing was performed by the Centre National de
               Sequencage (Genoscope, Evry, France)."
BASE COUNT    98 a 55 c 67 g 111 t
ORIGIN
Query Match   5.1%; Score 87; DB 9; Length 331;
Best Local Similarity 61.9%; Pred. No. 4e-14;
Matches 138; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

| Qy 613 AGGAATAAAGCTAATACCTGTCAGAGTGTGCGGCATTGACCAATGAGATCACA 672
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 308 AGCACTCGGACCTTCCATTTCAAGATATCTGCAAGTGTAGACCAATGATATATCA 249
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Qy 673 AGCATGGCAAGATGGCAATCTCGGCAAGGACGGAATATATGTTACTACTACATCG 732
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 248 AGCATTTGGTGGTAAATGTGACAAAGAGTGTCACAATATTTGTAACAACACCTCA 189
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Qy 733 AACAGGAACCATATCAATGTTGCGGCAGCAAGGACCCCGCAGATAGTTCCTGTTCTC 792
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 188 AATAGGAACCAATTAATGTTATCCCAAGCAAAACGCGATGATACATTTCTGTCCTC 129
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Qy 793 CACAGCAATATCCGAACCTGCATAGCTCCCAACATGAAT 835
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 128 CATATACATCATGAGCCACTTTTCTCCACCACCAAGATTTCAT 86

RESULT 4
LOCUS        BH885023/c
DEFINITION   BH885023
               hw55f08.b1 WGS-zmaysF (JM107 adapted methyl filtered) Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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genomic clone hw55f08 5', DNA sequence.
BH885023
VERSION      BH885023.1  GI:22120920
KEYWORDS     GSS.
SOURCE       Zea mays.
ORGANISM     Zea mays.
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 415)
AUTHORS      Rabinowicz,P.D., O'Shaughnessy,A.L., Ballia,V., Dedhia,N.,
               Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
               Zutaverni,F., McCombie,W.R. and Martienssen,R.A.
TITLE        Genomic shotgun sequences from Zea mays (methyl-filtered)
JOURNAL       Unpublished (2002)
COMMENT       Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mcombie@cshl.org
               Plate: hw55 row: f column: 08
               Seq primer: -21M13UnivFwd
               Class: shotgun
               High quality sequence stop: 415.
FEATURES      Location/Qualifiers
               source
               1..415
               /organism="Zea mays"
               /cultivar="B73"
               /db_xref="taxon:4577"
               /clone="hw55f08"
               /clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
               /lab_host="JM107 or DH5a"
               /note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
               The vector was digested with XbaI and one nucleotide was
               added by fill in in the recessive 3' end. The genomic DNA
               was nebulized, end repaired, adaptor ligated and size
               fractionated using sephadex. The resulting fragments were
               between 0.8 and 3 kb and were cloned into the vector
               (-xy) reads in M13mp19. -b/g reads in pUC19). The same
               ligation was transformed in either JM107 or DH5a."
BASE COUNT    98 a 124 c 88 g 105 t
ORIGIN
Query Match   5.1%; Score 85.8; DB 17; Length 415;
Best Local Similarity 67.8%; Pred. No. 1e-13;
Matches 120; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

| Qy 341 AACGTAGCAAGGAGTAGATATTATTATGTACACGAGGAATCTTTACAGATCCTTTCCACA 400
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 312 AAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 253
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Qy 401 TGCATGTCGTAAAGCAAGATACAGTGTAGCTAGTTAGTTGTAATGAGCGGTCATGCCAT 460
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 252 CGCAAGCTGTAGAGAGCGGATACAAAGTCAGCCAGTTGTATGGTGGTCCCGCAGC 193
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Qy 461 TTCTCTGAAGGATGTTTCAGAGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAA 517
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
| Db 192 TTCTTTGAACGGCTGTTCAGAAAGATCACCCTCCGGGATTTGTGGAGGCGCCTGCA 136
|      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
LOCUS        BH416345
DEFINITION   BH416345
               1007047F07.1EL_xl 1007 - RescueMu Grid H Zea mays genomic, DNA
               sequence.
ACCESSION    BH416345.1  GI:17598744
KEYWORDS     GSS.
SOURCE       Zea mays.
ORGANISM     Zea mays.
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 120)
AUTHORS
Walbot, V.
TITLE
Maize genomic sequences found using engineered RescueMu transposon
JOURNAL
unpublished (2001)
COMMENT
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007047 column: 14
Class: transposon-tagged.

```

Class: transposon-tagged
Location/Qualifiers
1. .120
/organism="zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - RescueMu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription web
units. For more information on RescueMu, go to the
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
25 a 25 c 33 g 37 t
BASE COUNT

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BASE COUNT      25 a      25 c      37 t
ORIGIN
Query Match      4.8%      Score 82.2;  DB 17;  Length 120;
Best Local Similarity 80.7%;  Pred. No. 6.2e-13;
Matches 96;  Conservative 0;  Mismatches 23;  Indels 0;  Gaps 0;

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362	Qy	TCTTCAGATCC	TTCCACATCAAT	CTCTCTAAAGACAGAT	CACAGTGTAGTTTGT	441
2	Db	TCCTTCAGATCC	TTCCCGCATCAAT	CTCATAAAGGGCAGCT	CGGTGTGTGCCACTTTGT	61
442	Qy	AATGGACG	TCAATGCCATTTCT	CTCAAGGCAGTGT	TCACAGAGATGATGATCTTCGGGATC	500
62	Db	AATGGATGATCT	GTGCTCTTTGTTCG	AAGGCAGTGTCT	CACAGAGATGATCACTTCTCGGATC	120

RESULT 6	EST 22-AUG-2002
BU014814/c	
LOCUS	654 bp mRNA linear
DEFINITION	QGJ8109.yg.abl QC_EFGHJ lettuce serriola <i>Lactuca sativa</i> cDNA clone
	OCJ8109.mRNA sequence.

ACCESSION BU014814
 VERSION BU014814.1 GI:22449209
 KEYWORDS EST.
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca.

REFERENCE
1 (bases 1 to 654)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L., and Bradford, K.

TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL	http://compenomics.ucdavis.edu/
COMMENT	Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Amundsen Hall, UCD Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.edu belongs to contig OG_CA_Contig7857, see http://cgpdb.ucdavis.edu/ for details.

FEATURES	source
Plate: QGJ8	Tov; H column; 09.
	Location/Qualifiers
	1. .654
	/organism="Lactuca sativa"
	/cultivar="L.serricola"
	/db_xref="taxon:4236"
	/clone="QGJ8H09"
	/clone_lib="QG_EFGHJ lettuce serricola"
	/lab_host="E.coli"
	/note="Vector: pBRCN4SfAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
	TAG_LIB-QG_EFGHJ lettuce serricola
	TAG_TISSUE-flowers pre-fertilized
	TAG_SEQ-ccttcacgcg"

BASE COUNT	162 a	151 c	152 g	189 t
ORIGIN				

Query Match	4.6%	Score 78.6;	DB 14;	Length 654;
Best Local Similarity	60.6%;	Pred. No. 1.5e-11;		
Matches 129;	Conservative	0;	Mismatches 84;	Indels 0;
Gaps	0;			

Qy	614	GGAANTAAAGCTTAATACCTGTCTCCAGAGCTGTGGCGGCATTTGACCAAAATGAGAGATCACAA	673
Db	505	GGAATTTGGTGGGACACTGTGTATGAACCTTTCGGCCATTTGGACCAACAGAAAGGACTG	446
Qy	674	GCATGGCAAGAATGGCAATCTGGCAAGGAGCGGGAATATATTTGTTATTTCTACTACATTCGA	733
Db	445	CTAGAGCTAAGATTTAGACTATGGCATACTAGTGAAGTAAAGTATATATACCAACCAACTCAA	386
Qy	734	ACAGGAACCATATCAATGTGTCGCCACAGCAAGACACCCCGCAGATAAGTTCTGTGTTCTTCC	793
Db	385	AAAGCACCATATCAATGTGCAAAACCCGAGCACAACCAACGAGAAAGCTTCTTGTGCTCTCC	326
Qy	794	ACAGCAGATATCCGCAACTGTCATAGCTCCCAA	826
Db	325	AGAGGAAGATATCACGAGTTTGGCGCTCTCTTA	293

RESULT 7	655 bp	linear	EST 14-AUG-2002
BQ854032/c			
LOCUS			
DEFINITION	BQ854032	lettuce <i>salinas</i>	Lactuca sativa cDNA clone
	CG822C16.v9.ab1		
	CG822C16		
			CG822C16 mRNA sequence.

ACCESSION BQ854032
VERSION BQ854032.1 GI:22239497
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 1 (bases 1 to 655)
 KOZIK A., MICHELMORE, R.W., KNAPP, S., MATVIENKO, M., RIESEBERG, L.,
 CRONIN 1999

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://comgenomics.ucdavis.edu/>
Unpublished (2002)

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
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Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
singleton, see <http://cgdb.ucdavis.edu/> for details.
Plate: OGB22 row: C column: 16.

FEATURES

source

1. 655
/organism="Lactuca sativa"
/cultivar="salinas"
/db_xref="taxon:4236"
/clone="QG22C16"
/lab_host="E.coli"
/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that directionally cloned into a custom medium-copy vector and size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG LIB-QG-ABCDI lettuce salinas
TAG TISSUE-flowers post-fertilized
TAG_SEQ-TGCCATCGG"

BASE COUNT 176 a 124 c 153 g 202 t
ORIGIN

Query Match 4.6%; Score 78.6; DB 14; Length 655;
Best Local Similarity 62.4%; Pred. No. 1.6e-11;
Matches 123; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 614 GGAATAAGCTAATACCTCTCCAGAGTGGTGGCGCATTTGACCAATGAAGATCACAA 673
DB 416 GGATTTTGGTGAGATTGTTGATGAAGCTGAGCGATTGACCATAGAAATAGTATTG 357
QY 674 GCATGGCAGANTGGCAATCTGCCAAGGAGCGGAATATATTCTACTACATCGA 733
DB 356 CCAATGTAAAGATCAGACTGTGCAACAAAGTGTCCAGCAGATGATATTTCCATCACTCAA 297
QY 734 ACAGGAACCATATCAATGTTGCCCGCAGCAAGACCCCGCAGATAAGTCTCTCTTCC 793
DB 296 AAGGAACCATGATGTTGAAACTCCACCTPAGCATTTCCACCAGATACCTTCTTCTCTCC 237
QY 794 ACAGCAGAAATATCGCA 810
DB 236 ATAGGAGCAGATCGGCA 220

RESULT 8
BU010172/c
LOCUS BU010172 670 bp mRNA linear EST 22-AUG-2002
DEFINITION QGJ12K14.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
LOCUS QGJ12K14, mRNA sequence.

ACCESSION BU010172
VERSION BU010172.1 GI:22444567
KEYWORDS EST.

SOURCE

Lactuca sativa.

ORGANISM

Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

REFERENCE

AUTHORS

1. (bases 1 to 670)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://comgenomics.ucdavis.edu/>
Unpublished (2002)

JOURNAL

COMMENT

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Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7857, see <http://cgdb.ucdavis.edu/> for details.
Plate: OGB12 row: K column: 14.

FEATURES

source

1. 670
/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGJ12K14"
/lab_host="E.coli"
/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG LIB-QG_EFGHJ lettuce serriola
TAG TISSUE-flowers pre-fertilized
TAG_SEQ-CTTTGACGGG"

BASE COUNT 166 a 151 c 156 g 197 t
ORIGIN

Query Match 4.6%; Score 78.6; DB 14; Length 670;
Best Local Similarity 60.6%; Pred. No. 1.7e-11;
Matches 129; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 614 GGAATAAGCTAATACCTCTCCAGAGTGGTGGCGCATTTGACCAATGAAGATCACAA 673
DB 501 GGAATCTTTGGTGAGACTTGTGATGAAGCTTGGCGCATTTGCCACAGAAAAGACTG 442
QY 674 GCATGGCAGAAATGGCAATCTGGCAAGGAGCGGAATATATTGTATTCTACTACATCGA 733
DB 441 CTAGAGCTTAAGATTAGAGTATGGCATACTAGTGTAAAGTAAATATTTCAACCAACTCA 382
QY 734 ACAGGAACCATATCAATGTTGCCCGCAGCAAGACCCCGCAGATAAGTTCCTCTCTCC 793
DB 381 AAAGCAGCCATATCAATGTGGCAACCCGAGCAGACACCATCTTCTTCTCTCC 322
QY 794 ACAGCAGAAATATCTCCGCAACTGCATAGCTCCCAA 826
DB 321 AGAGGAAGATATACGACAGGTTTCCCGCTCCTTA 289

RESULT 9

BU000882/c

LOCUS

QGS26E24.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone

DEFINITION

QGS26E24, mRNA sequence.

ACCESSION

BU000882

VERSION

BU000882.1 GI:22435277

KEYWORDS

EST.

SOURCE

Lactuca sativa.

ORGANISM

Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

REFERENCE

1 (bases 1 to 712)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolman, J., Stabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, J., and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
Unpublished (2002)

TITLE

Letuce and Sunflower ESTs from the Compositae Genome Project

JOURNAL

Unpublished (2002)

COMMENT

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Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozikeatgc.org [michelmore@vegmall.ucdavis.edu]
belongs to contig OG_CA_Contig7857, see http://cgdb.ucdavis.edu/
for details.
Plate: QGG26 row: E column: 24.

FEATURES

Location/Qualifiers
1..712
/organism="Lactuca sativa"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGG2624"
/lab_host="E.coli"
/note="vector: pBRCDNA5FIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_SEQ=Not found"

BASE COUNT 177 a 148 c 163 g 224 t
ORIGIN

Query Match 4.6%; Score 78.6; DB 14; Length 712;
Best Local Similarity 62.4%; Pred. No. 1.7e-11;
Matches 123; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 614 GGAATAAAGCTATACCTGTCACAGAGTGTGGCGCATTTGACCAATGAAGATCAAA 673
Db 244 GGAACCTTGGTGAGACTTGTGTAGTGAAGCTTGGCGCATTTGACCAATGAAGAGTGTG 185
Qy 674 GCATGCAAGATGGCAATCTGCGCAAGAGCGGAATTTATTTGTTTCTACTACATCGA 733
Db 184 CTAGAGTAAGATTAGAGTATGGCATACTAGTCTAAGTAAGTATTAATCAACCAACTCAA 125
Qy 734 ACAGGAACCATATCAATGTCGCCACAGAGGCCCGCCAGATAGTTCTGTTCTTCC 793
Db 124 AAAGCACCATATCAATGTCGCAAAACCGAGCACACGAGAAACCTTCTTGTCTTCC 65
Qy 794 ACAGCAGATATCCGCA 810
Db 64 AGAGGAAGATATCAGCA 48

RESULT 10

BU012310/c
LOCUS BU012310 732 bp mRNA linear EST 22-AUG-2002
DEFINITION OGJ08.yg.abl OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
BU012310
ACCESSION BU012310.1 GI:22446705
VERSION BU012310.1
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 732)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolman, J., Stabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, J., and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
Unpublished (2002)

COMMENT

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Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozikeatgc.org [michelmore@vegmall.ucdavis.edu]
belongs to contig OG_CA_Contig7857, see http://cgdb.ucdavis.edu/
for details.
Plate: QGJ1 row: J column: 08.

FEATURES

Location/Qualifiers
1..732
/organism="Lactuca sativa"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGJ1J08"
/lab_host="E.coli"
/note="vector: pBRCDNA5FIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_SEQ=Not found"

BASE COUNT 181 a 167 c 170 g 214 t
ORIGIN

Query Match 4.6%; Score 78.6; DB 14; Length 732;
Best Local Similarity 60.6%; Pred. No. 1.7e-11;
Matches 129; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 614 GGAATAAAGCTATACCTGTCACAGAGTGTGGCGCATTTGACCAATGAAGATCAAA 673
Db 537 GGAACCTTGGTGAGACTTGTGTAGTGAAGCTTGGCGCATTTGACCAATGAAGAGTGTG 478
Qy 674 GCATGCAAGATGGCAATCTGCGCAAGAGCGGAATTTATTTGTTTCTACTACATCGA 733
Db 477 CTAGAGTAAGATTAGAGTATGGCATACTAGTCTAAGTAAGTATTAATCAACCAACTCAA 418
Qy 734 ACAGGAACCATATCAATGTCGCCACAGAGGCCCGCCAGATAGTTCTGTTCTTCC 793
Db 417 AAAGCACCATATCAATGTCGCAAAACCGAGCACACGAGAAACCTTCTTGTCTTCC 358
Qy 794 ACAGCAGATATCCGCAACTGCATAGCTCCCAA 826
Db 357 AGAGGAAGATATCAGCAGTTTGGCGCTCTCTA 325

RESULT 11

BU014761/c
LOCUS BU014761 744 bp mRNA linear EST 22-AUG-2002
DEFINITION OGJ8E16.yg.abl OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
BU014761
ACCESSION BU014761
VERSION BU014761
KEYWORDS EST.
SOURCE Lactuca sativa.

DEFINITION QGF27F06.Y9.ab1 OG_EFGHJ lettuce serriola Lactuca sativa cdna clone
 LOCUS QGF27F06, mRNA sequence.
 ACCESSION BQ993006
 VERSION BQ993006.1 GI:22412541
 KEYWORDS EST.
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 REFERENCE 1 (bases 1 to 750)
 AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
 P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
 Church,S., Jackson,L. and Bradford,K.
 TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
 JOURNAL http://compgenomics.ucdavis.edu/
 COMMENT Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
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 Asmudson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig OG_CA_Contig7857, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: QGF27 row: F column: 06.
 FEATURES
 source Location/Qualifiers
 1..750
 /organism="Lactuca sativa"
 /cultivar="L.serriola"
 /db_xref="taxon:4236"
 /clone="QGF27F06"
 /clone_lib="OG_EFGHJ lettuce serriola"
 /lab_host="E.coli"
 /note="Vector: pBRCDNASFIAB: The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB-OG_EFGHJ lettuce serriola
 TAG_TISSUE=flowers environmental stress
 TAG_SEQ=CGAATCGGG"
 BASE COUNT 188 a 148 c 167 g 246 t 1 others
 ORIGIN
 Query Match 4.6%; Score 78.6; DB 14; Length 750;
 Best Local Similarity 60.6%; Pred. No. 1.8e-11;
 Matches 129; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 614 GGAATAAAGCTAATACCTGCCAAGAGTGTGGCGCATTTGACCAATGAAGATCAAA 673
 DB 271 GGAACCTTGGAGACTTGTGTAGTGAAGCTTGGCGCATTTGACCAAGAAAGGACTG 212
 QY 674 GCATGCAAGATGCAATCTGGCAAGAGGAGCGAATATATTGTATCTACTACATCGA 733
 DB 211 CTAGACTAGATTAGATATGGCATCTACTAGTAAAGTATGATATTCACCAACTCAA 152
 QY 734 ACAGGACCATATCAATCTTCCCCCAGCAAGACCCCGCAGATAGTTCCCTGTTCTTCC 793
 DB 151 AAAGCACCATTATCAATGTGGCAAAACCCGAGCACACAGCAGAAACCTTCTTCTTCC 92
 QY 794 ACAGGAGATATCCGCAACTGCATAGCTCCCAA 826
 DB 91 AGAGGAAGATATCAGCAGGTTTGGCGGCTCCTA 59

RESULT 14
 BQ853513/c
 LOCUS QGB20L12.Y9.ab1 OG_ABCDI lettuce salinas Lactuca sativa cdna clone
 DEFINITION QGB20L12, mRNA sequence.
 ACCESSION BQ853513
 VERSION BQ853513.1 GI:22238978
 KEYWORDS EST.
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 REFERENCE 1 (bases 1 to 762)
 AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
 P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
 Church,S., Jackson,L. and Bradford,K.
 TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
 JOURNAL http://compgenomics.ucdavis.edu/
 COMMENT Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmudson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig OG_CA_Contig7857, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: QGB20 row: L column: 12.
 FEATURES
 source Location/Qualifiers
 1..762
 /organism="Lactuca sativa"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGB20L12"
 /clone_lib="OG_ABCDI lettuce salinas"
 /lab_host="E.coli"
 /note="Vector: pBRCDNASFIAB: The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB-OG_ABCDI lettuce salinas
 TAG_TISSUE=roots
 TAG_SEQ=GTTCGACGGG"
 BASE COUNT 192 a 149 c 167 g 254 t
 ORIGIN
 Query Match 4.6%; Score 78.6; DB 14; Length 762;
 Best Local Similarity 60.6%; Pred. No. 1.8e-11;
 Matches 129; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 614 GGAATAAAGCTAATACCTGCCAAGAGTGTGGCGCATTTGACCAATGAAGATCAAA 673
 DB 238 GGAACCTTGGTGAGACTTGTGTAGTGAAGCTTGGCGCATTTGACCAAGAAAGGACTG 179
 QY 674 GCATGCAAGATGCAATCTGGCAAGAGGAGCGAATATATTGTATCTACTACATCGA 733
 DB 178 CTAGACTAAGATTAGATATGGCATCTACTAGTAAAGTATGATATTCACCAACTCAA 119
 QY 734 ACAGGACCATATCAATCTTCCCCCAGCAAGACCCCGCAGATAGTTCCCTGTTCTTCC 793
 DB 118 AAAGCACCATTATCAATCTGCGCAAAACCCGAGCACACAGCAGAAACCTTCTTCTTCC 59
 QY 794 ACAGCAGATATCCGCAACTGCATAGCTCCCAA 826

Db 58 AGAGGAAGATATCAGCAGCGTTTGGCGCTCCTA 26

RESULT 15

LOCUS BG462180/c

DEFINITION BG462180 512 bp mRNA linear EST 20-MAR-2001
947047F08.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
sequence.

ACCESSION BG462180

VERSION BG462180.1 GI:13388469

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 512)

Wolbot.V.

Maize ESTs from various cDNA libraries sequenced at Stanford

Unpublished (1999)

Contact: Wolbot.V.

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: wolbot@stanford.edu

Plate: 947047 row: F column: 08.

Location/Qualifiers

1. .512

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone_lib="947 - 2 week shoot from Barkan lab"

/tissue_type="leaf and stem, including leaf base"

/dev_stage="2 week old seedling (3 leaves)"

/lab_host="XLI-Blue"

/note="Organ: shoot; Vector: Lambda ZAP (pBluescript SK-);

Site1: EcoRI; Site2: XhoI; Directionally cloned using

Stratagene's Unizap XR cDNA cloning kit with the 5' end

at the EcoRI site. The library represents 8 x 10e5

independent recombinant phage. The plants were greenhouse

grown."

BASE COUNT 100 a 146 c 146 g 120 t

ORIGIN

Query Match 4.6%; Score 78; DB 12; Length 512;

Best Local Similarity 64.3%; Pred. No. 2.2e-11;

Matches 117; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 629 ACCTGTCACAGTGGTGGCGGATTGACCAATGAGATCACAGCATGGCAAGATGG 688

Db 435 ACTTTGTGATGAAGTGGAGGATGGACACAGAGAGATGGCCGAGGAGATGA 376

QY 689 CAATCTGCCAAGAGCGGAATTATATTGTATCTACTACATCGAACAGGAACCATATCA 748

Db 375 GACAGTGGCACACAGAGTGGAGAGATGGTACTCCATGACCTCGAATAGGAGCCAGATGG 316

QY 749 ATGTTGCCCGCAGACGACCCCGGAGATTAAGTTCTCTGTTCTTCCACAGCAGATATCCG 808

Db 315 CGGTGGCACCAGCAAGTACCCCGCAGAGATCTTCTCTCTCCATAGGATAAGATCGG 256

QY 809 CA 810

Db 255 CA 254

Search completed: December 2, 2002, 03:59:43
Job time : 2540.16 secs

1

2

3

4

5